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Gala, Jean-Luc

<120> GENETIC SEQUENCES, DIAGNOSTIC AND/OR QUANTIFICATION METHODS AND DEVICES
FOR THE IDENTIFICATION OF STAPHYLOCOCCI STRAINS

<130> VANM145.001APC

<140> 09/509,234

<141> 1998-09-28

<160> 64

<170> PatentIn version 3.0

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<212> DNA

<213> Staphylococcus femA Consensus Sequence

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nnannnnnnnn ganncncann tagtnggnat naanaanaan nataangang tnattgcngc	180
ntgnntntntn acngcngtnc cngtnatgaa antntttnaan tantttttatt cnaannnggg	240
nccngtnatn gattntnana annnaganct ngtncantnn ttctttaang antttnnnnaa	300
ntatntnaaa nannannntn nnntatannt nnnnntngan ccntanntnn cntatcaata	360
nnnnaatcat gangngann tnnnnngnaa tgcngggnan gattggntnt tngatnannt	420
nnnnnnnnntn ggntntnanc annnnnggntt nnnnannggn ttgancnccn tnnnncaa	480
nnngntnnan tcngtnntan atttannnnn naaaannncn nanganntnn tnaannnnat	540
ggatngnntn ngnaannnga anacnaaaaa agtnnanaan aatggngtna aagttnnnntt	600
nnnnnnnnnaa ganganntnc cnatnttnng ntcattnatg gangatacnn cnganncnaa	660
ngnnttnnnn gatngngang annnntnta ntanaanngn tnnnnnnatt nnaaagann	720
ngtnntngtn ccntngcnt atatnnantt tgatgantan ntnnnnnga tnnannnga	780
nngnnannnn ntnantaaag annnnaanaa agcnnntnaan ganatngana aangnccnga	840
naanaaaaaa gcnnnnnaa annnnnnnaa nntnnaanan caantnnng cnaannanca	900

aaanntnnan gangnnannn nnnntnaann nnancatggn aangaattac cnatntcngc	960
ngnntncttn ntnatnaatc cntntgaagt ngntntantan gcnggtggna cntcnaatnn	1020
ntnnngncan ttngcnggna gntatgcnt ncaatgggnn atgattaant atgcnntnna	1080
ncatnnnatn nanngntana atttntatgg nnttagnggt nantttanng angangcnga	1140
agatgnnggn gtnntnaant tnaaaaangg nttnnatgcn ganntnntng antangttgg	1200
nganttnntn aaaccnatna anaanccnnt ntannnnnnn tatannncan tnaaaaannt	1260
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gttaannn	1328

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 1 5 10 15

gat aag atg cca tat agt cat ttc aca caa atg act gaa aac tat gag 96
 Asp Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu
 20 25 30

atg aaa gtt gca aat aaa aca gaa act cac tta gtt ggt ata aaa aat 144
 Met Lys Val Ala Asn Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn
 35 40 45

aaa gat aat gag gtt att gca gcc tgc atg ttg aca gca gta cca gtc 192
 Lys Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val
 50 55 60

atg aaa ttt ttt aag tac ttt tat tct aac cga gga cct gta att gat 240
 Met Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
 65 70 75

tat gat aat aga gag ctt gtt cac ttt ttc ttt aat gag tta aca aag 288
 Tyr Asp Asn Arg Glu Leu Val His Phe Phe Phe Asn Glu Leu Thr Lys
 80 85 90 95

tat tta aaa cag cat aat tgt cta tat gtt cga gtt gac cct tat tta 336
 Tyr Leu Lys Gln His Asn Cys Leu Tyr Val Arg Val Asp Pro Tyr Leu
 100 105 110

cca tat caa tat tta aat cat gat ggt gaa att aca ggt aat gct ggt 384
 Pro Tyr Gln Tyr Leu Asn His Asp Gly Glu Ile Thr Gly Asn Ala Gly

115	120	125	
aat gat tgg ttc ttt gat aag atg aag cat ctc gga ttt gaa cat gaa Asn Asp Trp Phe Phe Asp Lys Met Lys His Leu Gly Phe Glu His Glu 130 135 140			432
ggc ttt act aaa ggt ttt gat ccg att aaa caa atc cga tat cat tct Gly Phe Thr Lys Gly Phe Asp Pro Ile Lys Gln Ile Arg Tyr His Ser 145 150 155			480
ggt tta gat tta aaa aat aaa aca tct aaa gat ata tta aat gga atg Val Leu Asp Leu Lys Asn Lys Thr Ser Lys Asp Ile Leu Asn Gly Met 160 165 170 175			528
gat agt cta cgt aaa cgt aat act aaa aaa gtt caa aaa aat ggt gtg Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val 180 185 190			576
aaa gtt aag ttc tta tca gaa gaa gaa ctt cca atc ttc cgt tca ttt Lys Val Lys Phe Leu Ser Glu Glu Glu Leu Pro Ile Phe Arg Ser Phe 195 200 205			624
atg gaa gat aca acc gaa acg aaa gaa ttc caa gat aga gat gat agt Met Glu Asp Thr Thr Glu Thr Lys Glu Phe Gln Asp Arg Asp Asp Ser 210 215 220			672
ttc tat tat aat cgc tat aga cat ttc aaa gat cac gtg ctt gta cca Phe Tyr Tyr Asn Arg Tyr Arg His Phe Lys Asp His Val Leu Val Pro 225 230 235			720
cta gct tat att aag ttt gat gag tac atc gaa gaa tta caa aat gaa Leu Ala Tyr Ile Lys Phe Asp Glu Tyr Ile Glu Glu Leu Gln Asn Glu 240 245 250 255			768
cgt gaa act tta aat aaa gat gtt aat aaa gct tta aaa gat att gaa Arg Glu Thr Leu Asn Lys Asp Val Asn Lys Ala Leu Lys Asp Ile Glu 260 265 270			816
aaa cga cca gac aat aaa aag gca ttt aat aaa aaa gaa aat ctt gaa Lys Arg Pro Asp Asn Lys Lys Ala Phe Asn Lys Lys Glu Asn Leu Glu 275 280 285			864
aaa caa tta gat gcc aat caa caa aaa tta gac gag gct aaa aaa tta Lys Gln Leu Asp Ala Asn Gln Gln Lys Leu Asp Glu Ala Lys Lys Leu 290 295 300			912
caa gcc gaa cat ggt aat gaa tta cca att tca gca ggt ttc ttc ttt Gln Ala Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe 305 310 315			960
att aat cca ttt gaa gtt gtt tat tat gca ggt gga act tct aat aaa Ile Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys 320 325 330 335			1008
tat aga cat ttt gca ggc agt tat gct att caa tgg aca atg att aac Tyr Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Thr Met Ile Asn 340 345 350			1056

tat gca att gat cat ggt att gat aga tac aat ttc tat ggt att agc	1104
Tyr Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser	
355 360 365	

ggt aat ttt agt gaa gac gct gaa gat gtt gga gtc att aaa ttt aaa	1152
Gly Asn Phe Ser Glu Asp Ala Glu Asp Val Gly Val Ile Lys Phe Lys	
370 375 380	

aaa ggt ttc aat gca gac gta att gag tat gtt gga gac ttt gtg aaa	1200
Lys Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys	
385 390 395	

cct att aac aaa cct ttg tat tca gtg tat aag aca ctc aaa aag att	1248
Pro Ile Asn Lys Pro Leu Tyr Ser Val Tyr Lys Thr Leu Lys Lys Ile	
400 405 410 415	

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Lys Lys Arg Phe Asn	
420	

gagttaaac	1305
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20 25 30

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35 40 45

Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val Met
50 55 60

Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr
65 70 75 80

Asp Asn Arg Glu Leu Val His Phe Phe Phe Asn Glu Leu Thr Lys Tyr
85 90 95

Leu Lys Gln His Asn Cys Leu Tyr Val Arg Val Asp Pro Tyr Leu Pro
100 105 110

Tyr Gln Tyr Leu Asn His Asp Gly Glu Ile Thr Gly Asn Ala Gly Asn
 115 120 125

Asp Trp Phe Phe Asp Lys Met Lys His Leu Gly Phe Glu His Glu Gly
 130 135 140

Phe Thr Lys Gly Phe Asp Pro Ile Lys Gln Ile Arg Tyr His Ser Val
 145 150 155 160

Leu Asp Leu Lys Asn Lys Thr Ser Lys Asp Ile Leu Asn Gly Met Asp
 165 170 175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
 180 185 190

Val Lys Phe Leu Ser Glu Glu Glu Leu Pro Ile Phe Arg Ser Phe Met
 195 200 205

Glu Asp Thr Thr Glu Thr Lys Glu Phe Gln Asp Arg Asp Asp Ser Phe
 210 215 220

Tyr Tyr Asn Arg Tyr Arg His Phe Lys Asp His Val Leu Val Pro Leu
 225 230 235 240

Ala Tyr Ile Lys Phe Asp Glu Tyr Ile Glu Glu Leu Gln Asn Glu Arg
 245 250 255

Glu Thr Leu Asn Lys Asp Val Asn Lys Ala Leu Lys Asp Ile Glu Lys
 260 265 270

Arg Pro Asp Asn Lys Lys Ala Phe Asn Lys Lys Glu Asn Leu Glu Lys
 275 280 285

Gln Leu Asp Ala Asn Gln Gln Lys Leu Asp Glu Ala Lys Lys Leu Gln
 290 295 300

Ala Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe Ile
 305 310 315 320

Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys Tyr
 325 330 335

Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Thr Met Ile Asn Tyr
 340 345 350

Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
 355 360 365

Asn Phe Ser Glu Asp Ala Glu Asp Val Gly Val Ile Lys Phe Lys Lys
 370 375 380

Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys Pro
 385 390 395 400

Ile Asn Lys Pro Leu Tyr Ser Val Tyr Lys Thr Leu Lys Lys Ile Lys
 405 410 415

Lys Arg Phe Asn
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<220>
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ttt act caa atg aca ggt aac tat aat tta aaa gtt gcc gaa aaa aca	96
Phe Thr Gln Met Thr Gly Asn Tyr Asn Leu Lys Val Ala Glu Lys Thr	
20 25 30	
gaa aca cat tta gtt ggt gtt aaa aat aat aat aac gaa gta att gca	144
Glu Thr His Leu Val Gly Val Lys Asn Asn Asn Asn Glu Val Ile Ala	
35 40 45	
gca tgt tta ttg aca gct gta cca gtc atg aag ttt ttt aaa tac ttt	192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe	
50 55 60	
tac agc aat aga ggc cca gtt ata gat tat gct aac caa gaa ctt gta	240
Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Ala Asn Gln Glu Leu Val	
65 70 75 80	
cat ttt ttc ttt aat gag cta act aaa tat tta aaa aag tat aac tgt	288
His Phe Phe Phe Asn Glu Leu Thr Lys Tyr Leu Lys Lys Tyr Asn Cys	

85										90					95					
ctc	tat	gtc	cgc	ata	gat	cca	tac	tta	cct	tat	caa	tat	aga	gac	cat	336				
Leu	Tyr	Val	Arg	Ile	Asp	Pro	Tyr	Leu	Pro	Tyr	Gln	Tyr	Arg	Asp	His					
			100					105					110							
gac	ggt	aat	ata	acg	gca	aat	gct	ggc	aat	gat	tgg	ttt	ttc	aat	aaa	384				
Asp	Gly	Asn	Ile	Thr	Ala	Asn	Ala	Gly	Asn	Asp	Trp	Phe	Phe	Asn	Lys					
		115					120					125								
atg	gaa	caa	ctc	gga	tac	cat	cat	gat	ggc	ttt	aca	aca	gga	ttt	gat	432				
Met	Glu	Gln	Leu	Gly	Tyr	His	His	Asp	Gly	Phe	Thr	Thr	Gly	Phe	Asp					
	130					135					140									
cca	ata	tta	caa	atc	aga	ttc	cat	tct	att	ctt	aat	tta	aag	gat	aag	480				
Pro	Ile	Leu	Gln	Ile	Arg	Phe	His	Ser	Ile	Leu	Asn	Leu	Lys	Asp	Lys					
145				150					155						160					
aca	gct	aaa	gat	gtt	tta	aat	aat	atg	gat	agt	tta	cgt	aaa	aga	aat	528				
Thr	Ala	Lys	Asp	Val	Leu	Asn	Asn	Met	Asp	Ser	Leu	Arg	Lys	Arg	Asn					
				165				170					175							
acc	aaa	aaa	agt	tca	aaa	aat	gga	gtc	aaa	gta	aag	ttc	ctt	act	gaa	576				
Thr	Lys	Lys	Ser	Ser	Lys	Asn	Gly	Val	Lys	Val	Lys	Phe	Leu	Thr	Glu					
			180				185						190							
gaa	gaa	cta	cct	atc	ttt	cgt	tca	ttt	atg	gag	cag	acg	tca	gaa	tct	624				
Glu	Glu	Leu	Pro	Ile	Phe	Arg	Ser	Phe	Met	Glu	Gln	Thr	Ser	Glu	Ser					
		195					200					205								
aaa	gaa	ttc	tct	gat	aga	gac	gac	caa	ttt	tat	tac	aat	cgg	ttt	aag	672				
Lys	Glu	Phe	Ser	Asp	Arg	Asp	Asp	Gln	Phe	Tyr	Tyr	Asn	Arg	Phe	Lys					
	210					215					220									
tac	tat	aaa	gat	agg	gtg	ctt	gtg	cct	cta	gca	tat	tta	aaa	ttt	gat	720				
Tyr	Tyr	Lys	Asp	Arg	Val	Leu	Val	Pro	Leu	Ala	Tyr	Leu	Lys	Phe	Asp					
225				230				235							240					
gaa	tat	ata	gaa	gaa	cta	acg	aat	gaa	cga	caa	act	tta	gaa	aaa	gat	768				
Glu	Tyr	Ile	Glu	Glu	Leu	Thr	Asn	Glu	Arg	Gln	Thr	Leu	Glu	Lys	Asp					
			245					250						255						
tta	ggc	aaa	gca	ctt	aaa	gac	att	gag	aaa	cga	cca	gat	aac	aaa	aaa	816				
Leu	Gly	Lys	Ala	Leu	Lys	Asp	Ile	Glu	Lys	Arg	Pro	Asp	Asn	Lys	Lys					
			260				265						270							
gct	tat	aat	aaa	cga	gac	aac	cta	caa	caa	caa	ctc	gat	gcc	aat	caa	864				
Ala	Tyr	Asn	Lys	Arg	Asp	Asn	Leu	Gln	Gln	Gln	Gln	Leu	Asp	Ala	Asn					
		275				280						285								
caa	aag	tta	aat	gag	gct	aat	cag	tta	caa	gcg	gaa	cac	ggt	aat	gag	912				
Gln	Lys	Leu	Asn	Glu	Ala	Asn	Gln	Leu	Gln	Ala	Glu	His	Gly	Asn	Glu					
	290					295					300									
tta	cct	atc	tct	gcc	ggt	ttc	ttt	att	att	aat	ccg	ttt	gaa	gtt	gta	960				
Leu	Pro	Ile	Ser	Ala	Gly	Phe	Phe	Ile	Ile	Asn	Pro	Phe	Glu	Val	Val					
305				310				315							320					

tac tac gct gga ggt acc gct aat aaa tat cgt cat ttt gca ggt agt 1008
 Tyr Tyr Ala Gly Gly Thr Ala Asn Lys Tyr Arg His Phe Ala Gly Ser
 325 330 335

tac gcg gtt cag tgg act atg att aac tat gct atc gaa cac ggc ata 1056
 Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr Ala Ile Glu His Gly Ile
 340 345 350

gac aga tat aat ttc tac ggc att agt gga aac ttc tca gat gat gct 1104
 Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asn Phe Ser Asp Asp Ala
 355 360 365

gaa gac gca ggt gtc att cgc ttt aaa aaa ggt tat ggt gca gaa gtg 1152
 Glu Asp Ala Gly Val Ile Arg Phe Lys Lys Gly Tyr Gly Ala Glu Val
 370 375 380

att gaa tac gtt ggt gat ttt gta aaa cct ata aat aaa cct atg tat 1200
 Ile Glu Tyr Val Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Met Tyr
 385 390 395 400

aaa ctt tat tca gtg tta aaa cga att caa aat aag cta tag 1242
 Lys Leu Tyr Ser Val Leu Lys Arg Ile Gln Asn Lys Leu
 405 410

aggagaatgg attaattatg aaatttacag agtttaac 1280

<210> 43
 <211> 413
 <212> PRT
 <213> Staphylococcus lugdunensis femA

<400> 43

Thr Ala Asn Glu Phe Gly Asp Phe Thr Asp Gln Met Pro Tyr Ser His
 1 5 10 15

Phe Thr Gln Met Thr Gly Asn Tyr Asn Leu Lys Val Ala Glu Lys Thr
 20 25 30

Glu Thr His Leu Val Gly Val Lys Asn Asn Asn Asn Glu Val Ile Ala
 35 40 45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
 50 55 60

Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Ala Asn Gln Glu Leu Val
 65 70 75 80

His Phe Phe Phe Asn Glu Leu Thr Lys Tyr Leu Lys Lys Tyr Asn Cys
 85 90 95

Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Tyr Arg Asp His
100 105 110

Asp Gly Asn Ile Thr Ala Asn Ala Gly Asn Asp Trp Phe Phe Asn Lys
115 120 125

Met Glu Gln Leu Gly Tyr His His Asp Gly Phe Thr Thr Gly Phe Asp
130 135 140

Pro Ile Leu Gln Ile Arg Phe His Ser Ile Leu Asn Leu Lys Asp Lys
145 150 155 160

Thr Ala Lys Asp Val Leu Asn Asn Met Asp Ser Leu Arg Lys Arg Asn
165 170 175

Thr Lys Lys Ser Ser Lys Asn Gly Val Lys Val Lys Phe Leu Thr Glu
180 185 190

Glu Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Gln Thr Ser Glu Ser
195 200 205

Lys Glu Phe Ser Asp Arg Asp Asp Gln Phe Tyr Tyr Asn Arg Phe Lys
210 215 220

Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Leu Lys Phe Asp
225 230 235 240

Glu Tyr Ile Glu Glu Leu Thr Asn Glu Arg Gln Thr Leu Glu Lys Asp
245 250 255

Leu Gly Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
260 265 270

Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Gln Leu Asp Ala Asn Gln
275 280 285

Gln Lys Leu Asn Glu Ala Asn Gln Leu Gln Ala Glu His Gly Asn Glu
290 295 300

Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
305 310 315 320

Tyr Tyr Ala Gly Gly Thr Ala Asn Lys Tyr Arg His Phe Ala Gly Ser
325 330 335

Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr Ala Ile Glu His Gly Ile
340 345 350

Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asn Phe Ser Asp Asp Ala
355 360 365

Glu Asp Ala Gly Val Ile Arg Phe Lys Lys Gly Tyr Gly Ala Glu Val
370 375 380

Ile Glu Tyr Val Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Met Tyr
385 390 395 400

Lys Leu Tyr Ser Val Leu Lys Arg Ile Gln Asn Lys Leu
405 410

<210> 44
<211> 1295
<212> DNA
<213> Staphylococcus xylosus femA

<220>
<221> CDS
<222> (1)..(1245)

<400> 44
acg caa aag agt ttg ggt gca ttt tca gat aaa atg cca aat agc cat 48
Thr Gln Lys Ser Leu Gly Ala Phe Ser Asp Lys Met Pro Asn Ser His
1 5 10 15
ttc acg caa atg gta ggg aat tat gaa ttg aaa att gca gaa agt act 96
Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Ile Ala Glu Ser Thr
20 25 30
gaa aca cat tta gta ggt ata aaa aac aat gat aat gaa gtc att gca 144
Glu Thr His Leu Val Gly Ile Lys Asn Asn Asp Asn Glu Val Ile Ala
35 40 45
gct tgt tta tta act gca gta cca gta atg aaa ttc ttt aag tat ttt 192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
50 55 60
tat act aat aga ggt ccg gtt ata gat ttt gaa aat aaa gaa tta gtg 240
Tyr Thr Asn Arg Gly Pro Val Ile Asp Phe Glu Asn Lys Glu Leu Val
65 70 75 80
cat tac ttt ttc aat gaa cta tct aaa tat gtg aaa aaa cat aat gcg 288
His Tyr Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Ala

85										90					95					
ctt	tat	tta	aga	gtt	gat	cct	tat	tta	gca	tat	caa	tac	cgt	aat	cat	336				
Leu	Tyr	Leu	Arg	Val	Asp	Pro	Tyr	Leu	Ala	Tyr	Gln	Tyr	Arg	Asn	His					
100					105					110										
gat	ggt	gag	gta	ttg	gaa	aat	gca	gga	cat	gat	tgg	att	ttc	gat	aaa	384				
Asp	Gly	Glu	Val	Leu	Glu	Asn	Ala	Gly	His	Asp	Trp	Ile	Phe	Asp	Lys					
115					120					125										
atg	aag	cag	ctt	gga	tat	aaa	cac	caa	gga	ttt	tta	act	ggt	ttc	gat	432				
Met	Lys	Gln	Leu	Gly	Tyr	Lys	His	Gln	Gly	Phe	Leu	Thr	Gly	Phe	Asp					
130					135					140										
tca	att	att	caa	att	agg	ttc	cac	tct	gta	ctg	gat	tta	gta	ggt	aaa	480				
Ser	Ile	Ile	Gln	Ile	Arg	Phe	His	Ser	Val	Leu	Asp	Leu	Val	Gly	Lys					
145					150					155					160					
act	gct	aaa	gat	gta	cta	aat	ggt	atg	gat	agt	tta	cgt	aaa	cgt	aat	528				
Thr	Ala	Lys	Asp	Val	Leu	Asn	Gly	Met	Asp	Ser	Leu	Arg	Lys	Arg	Asn					
165					170					175										
act	aaa	aaa	gta	caa	aaa	aat	ggc	gtg	aaa	gta	agg	ttc	tta	agg	gaa	576				
Thr	Lys	Lys	Val	Gln	Lys	Asn	Gly	Val	Lys	Val	Arg	Phe	Leu	Arg	Glu					
180					185					190										
gat	gag	ttg	cca	att	ttc	cgt	tca	ttc	atg	gaa	gat	aca	tct	gaa	act	624				
Asp	Glu	Leu	Pro	Ile	Phe	Arg	Ser	Phe	Met	Glu	Asp	Thr	Ser	Glu	Thr					
195					200					205										
aaa	gac	ttt	gac	gat	aga	gac	gat	ggc	ttt	tac	tac	aat	aga	tta	agg	672				
Lys	Asp	Phe	Asp	Asp	Arg	Asp	Asp	Gly	Phe	Tyr	Tyr	Asn	Arg	Leu	Arg					
210					215					220										
tat	tat	aaa	gat	cgc	gta	tta	gta	cct	cta	gct	tat	atg	gat	ttc	aat	720				
Tyr	Tyr	Lys	Asp	Arg	Val	Leu	Val	Pro	Leu	Ala	Tyr	Met	Asp	Phe	Asn					
225					230					235					240					
gaa	tat	att	gaa	gaa	ttg	caa	gct	gaa	cgt	gag	gtg	tta	agc	aaa	gat	768				
Glu	Tyr	Ile	Glu	Glu	Leu	Gln	Ala	Glu	Arg	Glu	Val	Leu	Ser	Lys	Asp					
245					250					255										
atc	aat	aaa	gca	gta	aaa	gat	atc	gag	aaa	aga	cct	gaa	aat	aaa	aaa	816				
Ile	Asn	Lys	Ala	Val	Lys	Asp	Ile	Glu	Lys	Arg	Pro	Glu	Asn	Lys	Lys					
260					265					270										
gca	tat	aat	aaa	aaa	gat	aat	cta	gag	aaa	caa	ctt	ata	gcg	aat	caa	864				
Ala	Tyr	Asn	Lys	Lys	Asp	Asn	Leu	Glu	Lys	Gln	Leu	Ile	Ala	Asn	Gln					
275					280					285										
caa	aaa	att	gat	gaa	gct	aaa	act	cta	caa	gag	aag	cat	ggt	aac	gaa	912				
Gln	Lys	Ile	Asp	Glu	Ala	Lys	Thr	Leu	Gln	Glu	Lys	His	Gly	Asn	Glu					
290					295					300										
cta	cca	atc	tca	gca	gca	tat	ttc	atc	att	aac	cct	tat	gaa	gta	gtg	960				
Leu	Pro	Ile	Ser	Ala	Ala	Tyr	Phe	Ile	Ile	Asn	Pro	Tyr	Glu	Val	Val					
305					310					315					320					

tat tat gcg ggt gga acg tca aat gag ttt aga cat ttt gct ggt agt Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe Arg His Phe Ala Gly Ser 325 330 335	1008
tat gcc att caa tgg aag atg att aac tat gct att gac cat aat att Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Ile Asp His Asn Ile 340 345 350	1056
gat aga tat aat ttt tat gga att agt ggt cat ttt aca gaa gat gca Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly His Phe Thr Glu Asp Ala 355 360 365	1104
gaa gat gcc ggt gta gtt aaa ttt aaa aaa gga ttt aat gcg gat gta Glu Asp Ala Gly Val Val Lys Phe Lys Lys Gly Phe Asn Ala Asp Val 370 375 380	1152
gtg gaa tat gtt ggt gat ttt att aaa cca atc aat aaa cca atg tac Val Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr 385 390 395 400	1200
aaa att tat acg aca tta aag aaa att aaa gat aaa aag aaa taa Lys Ile Tyr Thr Thr Leu Lys Lys Ile Lys Asp Lys Lys Lys 405 410	1245
acatttaata gaagggaact aagctagaat gaaatttaca gagttaaacc	1295

<210> 45
 <211> 414
 <212> PRT
 <213> Staphylococcus xylosus femA

<400> 45

Thr Gln Lys Ser Leu Gly Ala Phe Ser Asp Lys Met Pro Asn Ser His 1 5 10 15
Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Ile Ala Glu Ser Thr 20 25 30
Glu Thr His Leu Val Gly Ile Lys Asn Asn Asp Asn Glu Val Ile Ala 35 40 45
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe 50 55 60
Tyr Thr Asn Arg Gly Pro Val Ile Asp Phe Glu Asn Lys Glu Leu Val 65 70 75 80
His Tyr Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Ala 85 90 95

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala Tyr Gln Tyr Arg Asn His
 100 105 110

Asp Gly Glu Val Leu Glu Asn Ala Gly His Asp Trp Ile Phe Asp Lys
 115 120 125

Met Lys Gln Leu Gly Tyr Lys His Gln Gly Phe Leu Thr Gly Phe Asp
 130 135 140

Ser Ile Ile Gln Ile Arg Phe His Ser Val Leu Asp Leu Val Gly Lys
 145 150 155 160

Thr Ala Lys Asp Val Leu Asn Gly Met Asp Ser Leu Arg Lys Arg Asn
 165 170 175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Arg Glu
 180 185 190

Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
 195 200 205

Lys Asp Phe Asp Asp Arg Asp Asp Gly Phe Tyr Tyr Asn Arg Leu Arg
 210 215 220

Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Met Asp Phe Asn
 225 230 235 240

Glu Tyr Ile Glu Glu Leu Gln Ala Glu Arg Glu Val Leu Ser Lys Asp
 245 250 255

Ile Asn Lys Ala Val Lys Asp Ile Glu Lys Arg Pro Glu Asn Lys Lys
 260 265 270

Ala Tyr Asn Lys Lys Asp Asn Leu Glu Lys Gln Leu Ile Ala Asn Gln
 275 280 285

Gln Lys Ile Asp Glu Ala Lys Thr Leu Gln Glu Lys His Gly Asn Glu
 290 295 300

Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile Asn Pro Tyr Glu Val Val
 305 310 315 320

Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe Arg His Phe Ala Gly Ser
325 330 335

Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Ile Asp His Asn Ile
340 345 350

Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly His Phe Thr Glu Asp Ala
355 360 365

Glu Asp Ala Gly Val Val Lys Phe Lys Lys Gly Phe Asn Ala Asp Val
370 375 380

Val Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
385 390 395 400

Lys Ile Tyr Thr Thr Leu Lys Lys Ile Lys Asp Lys Lys Lys
405 410

<210> 46
<211> 1283
<212> DNA
<213> Staphylococcus capitis femA

<220>
<221> CDS
<222> (1)..(1236)

<400> 46
aca gct aaa gaa ttt agt gac ttt act gat caa atg cct tat agc cat 48
Thr Ala Lys Glu Phe Ser Asp Phe Thr Asp Gln Met Pro Tyr Ser His
1 5 10 15

ttt act cag atg gaa ggt aat tat gaa ctt aaa gtt gct gaa ggt acg 96
Phe Thr Gln Met Glu Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Thr
20 25 30

gat tca cat ctc gta gga att aaa aat aat gac aac caa gtg att gca 144
Asp Ser His Leu Val Gly Ile Lys Asn Asn Asp Asn Gln Val Ile Ala
35 40 45

gca tgt tta tta act gct gta cct gta atg aaa att ttt aaa tat ttt 192
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Ile Phe Lys Tyr Phe
50 55 60

tac tca aat cgc ggg cca gtg att gat tat gat aat aaa gag ctt gtt 240
Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Asp Asn Lys Glu Leu Val
65 70 75 80

cac ttt ttc ttt aat gaa tta agt aaa tat gta aaa aag cat aat tgt 288
His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Cys

85					90					95						
ctt	tat	cta	aga	gtt	gac	cct	tat	ctt	cct	tat	caa	tac	tta	aat	cat	336
Leu	Tyr	Leu	Arg	Val	Asp	Pro	Tyr	Leu	Pro	Tyr	Gln	Tyr	Leu	Asn	His	
			100						105					110		
gac	ggt	gaa	att	att	gga	aat	gct	ggc	cat	gat	tgg	ttt	ttc	aat	aag	384
Asp	Gly	Glu	Ile	Ile	Gly	Asn	Ala	Gly	His	Asp	Trp	Phe	Phe	Asn	Lys	
		115					120					125				
atg	gaa	gaa	tta	gga	ttt	gaa	cat	gaa	ggc	ttt	cat	aaa	ggc	ttc	cat	432
Met	Glu	Glu	Leu	Gly	Phe	Glu	His	Glu	Gly	Phe	His	Lys	Gly	Phe	His	
	130					135					140					
cct	atc	tta	caa	gta	aga	tat	cat	tca	gtt	tta	gat	tta	aaa	gat	aaa	480
Pro	Ile	Leu	Gln	Val	Arg	Tyr	His	Ser	Val	Leu	Asp	Leu	Lys	Asp	Lys	
145					150					155					160	
acg	gct	aaa	gat	gta	ctc	aaa	gga	atg	gat	agt	tta	aga	aag	cgt	aat	528
Thr	Ala	Lys	Asp	Val	Leu	Lys	Gly	Met	Asp	Ser	Leu	Arg	Lys	Arg	Asn	
				165					170					175		
act	aag	aaa	gta	caa	aaa	aat	ggt	gtc	aaa	gtc	cgt	ttc	cta	tcc	gaa	576
Thr	Lys	Lys	Val	Gln	Lys	Asn	Gly	Val	Lys	Val	Arg	Phe	Leu	Ser	Glu	
			180					185					190			
gat	gaa	tta	cct	atc	ttt	aga	tca	ttt	atg	gaa	gat	act	aca	gaa	acg	624
Asp	Glu	Leu	Pro	Ile	Phe	Arg	Ser	Phe	Met	Glu	Asp	Thr	Thr	Glu	Thr	
		195					200					205				
aaa	gag	ttc	gcc	gat	aga	gat	gat	agt	ttc	tat	tat	aat	cga	tta	aaa	672
Lys	Glu	Phe	Ala	Asp	Arg	Asp	Asp	Ser	Phe	Tyr	Tyr	Asn	Arg	Leu	Lys	
	210					215					220					
tac	ttt	aaa	gat	aga	gta	tta	gta	cca	tta	gca	tat	gtt	gac	ttc	gat	720
Tyr	Phe	Lys	Asp	Arg	Val	Leu	Val	Pro	Leu	Ala	Tyr	Val	Asp	Phe	Asp	
225					230					235					240	
gag	tat	att	gaa	gaa	ctt	aat	aat	gaa	aga	gat	gtt	ctt	aat	aaa	gat	768
Glu	Tyr	Ile	Glu	Glu	Leu	Asn	Asn	Glu	Arg	Asp	Val	Leu	Asn	Lys	Asp	
			245					250						255		
tta	aat	aag	gcg	ctc	aaa	gat	att	gag	aag	aga	cct	gat	aat	aag	aaa	816
Leu	Asn	Lys	Ala	Leu	Lys	Asp	Ile	Glu	Lys	Arg	Pro	Asp	Asn	Lys	Lys	
			260					265					270			
gct	tat	aac	aaa	aga	gat	aat	ctt	caa	caa	caa	tta	gat	gca	aat	caa	864
Ala	Tyr	Asn	Lys	Arg	Asp	Asn	Leu	Gln	Gln	Gln	Leu	Asp	Ala	Asn	Gln	
		275					280					285				
caa	aaa	att	gat	gaa	gct	aaa	aac	tta	caa	caa	gaa	cat	ggt	aat	gaa	912
Gln	Lys	Ile	Asp	Glu	Ala	Lys	Asn	Leu	Gln	Gln	Glu	His	Gly	Asn	Glu	
	290					295					300					
tta	cct	att	tca	gct	gga	tat	ttc	ttc	att	aat	ccg	ttt	gaa	gtt	gtt	960
Leu	Pro	Ile	Ser	Ala	Gly	Tyr	Phe	Phe	Ile	Asn	Pro	Phe	Glu	Val	Val	
305					310					315					320	

tat tac gca ggt ggc aca tcg aat cgt tat cgt cac tat gcc gga agt	1008
Tyr Tyr Ala Gly Gly Thr Ser Asn Arg Tyr Arg His Tyr Ala Gly Ser	
325 330 335	

tat gca att caa tgg aaa atg ata aac tat gct tta gaa cat gga att	1056
Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Leu Glu His Gly Ile	
340 345 350	

aac cgt tat aat ttt tat gga gtt agt ggg gac ttc agt gaa gac gct	1104
Asn Arg Tyr Asn Phe Tyr Gly Val Ser Gly Asp Phe Ser Glu Asp Ala	
355 360 365	

gaa gat gta gga gta att aag ttc aaa aaa ggc tat aat gct gat gtt	1152
Glu Asp Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val	
370 375 380	

att gaa tat gta ggt gat ttt atc aag cca atc aat aaa cct atg tat	1200
Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr	
385 390 395 400	

gca atc tat aac gca ctt aaa aag tta aag aaa tag atttttttac	1246
Ala Ile Tyr Asn Ala Leu Lys Lys Leu Lys Lys	
405 410	

caaccctaatt atctaattat gaaatttaca gagttaa	1283
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<210> 47
 <211> 411
 <212> PRT
 <213> Staphylococcus capitis femA

<400> 47

Thr Ala Lys Glu Phe Ser Asp Phe Thr Asp Gln Met Pro Tyr Ser His
1 5 10 15

Phe Thr Gln Met Glu Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Thr
20 25 30

Asp Ser His Leu Val Gly Ile Lys Asn Asn Asp Asn Gln Val Ile Ala
35 40 45

Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Ile Phe Lys Tyr Phe
50 55 60

Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr Asp Asn Lys Glu Leu Val
65 70 75 80

His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys His Asn Cys
85 90 95

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Tyr Gln Tyr Leu Asn His
100 105 110

Asp Gly Glu Ile Ile Gly Asn Ala Gly His Asp Trp Phe Phe Asn Lys
115 120 125

Met Glu Glu Leu Gly Phe Glu His Glu Gly Phe His Lys Gly Phe His
130 135 140

Pro Ile Leu Gln Val Arg Tyr His Ser Val Leu Asp Leu Lys Asp Lys
145 150 155 160

Thr Ala Lys Asp Val Leu Lys Gly Met Asp Ser Leu Arg Lys Arg Asn
165 170 175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Glu
180 185 190

Asp Glu Leu Pro Ile Phe Arg Ser Phe Met Glu Asp Thr Thr Glu Thr
195 200 205

Lys Glu Phe Ala Asp Arg Asp Asp Ser Phe Tyr Tyr Asn Arg Leu Lys
210 215 220

Tyr Phe Lys Asp Arg Val Leu Val Pro Leu Ala Tyr Val Asp Phe Asp
225 230 235 240

Glu Tyr Ile Glu Glu Leu Asn Asn Glu Arg Asp Val Leu Asn Lys Asp
245 250 255

Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys Arg Pro Asp Asn Lys Lys
260 265 270

Ala Tyr Asn Lys Arg Asp Asn Leu Gln Gln Gln Leu Asp Ala Asn Gln
275 280 285

Gln Lys Ile Asp Glu Ala Lys Asn Leu Gln Gln Glu His Gly Asn Glu
290 295 300

Leu Pro Ile Ser Ala Gly Tyr Phe Phe Ile Asn Pro Phe Glu Val Val
305 310 315 320

Tyr Tyr Ala Gly Gly Thr Ser Asn Arg Tyr Arg His Tyr Ala Gly Ser
 325 330 335

Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr Ala Leu Glu His Gly Ile
 340 345 350

Asn Arg Tyr Asn Phe Tyr Gly Val Ser Gly Asp Phe Ser Glu Asp Ala
 355 360 365

Glu Asp Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val
 370 375 380

Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Met Tyr
 385 390 395 400

Ala Ile Tyr Asn Ala Leu Lys Lys Leu Lys Lys
 405 410

<210> 48
 <211> 1297
 <212> DNA
 <213> Staphylococcus schleiferi femA

<220>
 <221> CDS
 <222> (1)..(1248)

<400> 48
 acg acg gct gaa ttt ggt gcg ttt aca gat caa atg cca tat agc cat 48
 Thr Thr Ala Glu Phe Gly Ala Phe Thr Asp Gln Met Pro Tyr Ser His
 1 5 10 15
 ttc acg caa atg gta ggg aac tat gaa tta aag gtt gct gaa ggt gtt 96
 Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Val
 20 25 30
 gaa aca cat ctt gtc ggc att aaa gat aac aac aat aac gta cta gca 144
 Glu Thr His Leu Val Gly Ile Lys Asp Asn Asn Asn Asn Val Leu Ala
 35 40 45
 gca tgt tta ctg aca gca gtg cca gta atg aag ttt ttt aaa tat ttt 192
 Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe
 50 55 60
 tat tca aac cgc gga cca gtc atg gac tac gaa aat aaa gag ctc gtt 240
 Tyr Ser Asn Arg Gly Pro Val Met Asp Tyr Glu Asn Lys Glu Leu Val
 65 70 75 80
 cat ttc ttt ttt aat gaa ctt tca aaa tat gtt aag aaa tat cac gca 288
 His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys Tyr His Ala

85										90										95										
ttg	tat	ttg	aga	gta	gac	cct	tat	tta	cca	atg	tta	aag	cga	aac	cat		336													
Leu	Tyr	Leu	Arg	Val	Asp	Pro	Tyr	Leu	Pro	Met	Leu	Lys	Arg	Asn	His															
			100					105					110																	
gat	ggt	gaa	gtg	att	gaa	aga	tac	ggc	agt	gac	tgg	ttt	ttt	gat	aaa		384													
Asp	Gly	Glu	Val	Ile	Glu	Arg	Tyr	Gly	Ser	Asp	Trp	Phe	Phe	Asp	Lys															
		115					120					125																		
atg	gct	gaa	tta	aac	ttt	gaa	cat	gaa	ggt	ttc	aca	act	ggg	ttt	gat		432													
Met	Ala	Glu	Leu	Asn	Phe	Glu	His	Glu	Gly	Phe	Thr	Thr	Gly	Phe	Asp															
	130					135					140																			
aca	ata	agg	caa	att	cgt	ttt	cat	tct	gtg	ctc	gat	gtt	gaa	aat	aaa		480													
Thr	Ile	Arg	Gln	Ile	Arg	Phe	His	Ser	Val	Leu	Asp	Val	Glu	Asn	Lys															
	145				150					155					160															
aca	tca	aaa	gac	atc	tta	aat	caa	atg	gat	aat	tta	agg	aaa	aga	aat		528													
Thr	Ser	Lys	Asp	Ile	Leu	Asn	Gln	Met	Asp	Asn	Leu	Arg	Lys	Arg	Asn															
			165					170					175																	
acg	aaa	aaa	gta	cag	aaa	aat	ggt	gtg	aaa	gtc	cgc	tat	cta	aac	gaa		576													
Thr	Lys	Lys	Val	Gln	Lys	Asn	Gly	Val	Lys	Val	Arg	Tyr	Leu	Asn	Glu															
			180				185						190																	
gat	gaa	tta	cat	att	ttc	cgt	tcg	ttt	atg	gaa	gat	aca	tct	gaa	aca		624													
Asp	Glu	Leu	His	Ile	Phe	Arg	Ser	Phe	Met	Glu	Asp	Thr	Ser	Glu	Thr															
		195				200						205																		
aaa	gat	ttt	gta	gat	aga	gat	gac	gat	ttt	tat	tat	cat	cgt	atg	aaa		672													
Lys	Asp	Phe	Val	Asp	Arg	Asp	Asp	Asp	Phe	Tyr	Tyr	His	Arg	Met	Lys															
	210					215					220																			
tac	tat	aaa	gat	cgt	gtc	cgc	gta	cca	cta	gcg	tat	att	gat	ttt	aat		720													
Tyr	Tyr	Lys	Asp	Arg	Val	Arg	Val	Pro	Leu	Ala	Tyr	Ile	Asp	Phe	Asn															
	225			230					235						240															
gca	tat	tta	gca	gag	ctc	aac	act	gaa	gcg	caa	gac	ttt	aaa	aaa	gaa		768													
Ala	Tyr	Leu	Ala	Glu	Leu	Asn	Thr	Glu	Ala	Gln	Asp	Phe	Lys	Lys	Glu															
			245					250					255																	
att	gca	aaa	gca	gat	aaa	gac	atc	gac	aag	cgt	cct	gaa	aat	cag	aaa		816													
Ile	Ala	Lys	Ala	Asp	Lys	Asp	Ile	Asp	Lys	Arg	Pro	Glu	Asn	Gln	Lys															
			260				265						270																	
gcc	ata	aat	aaa	aag	aaa	aat	tta	gag	caa	caa	cta	gaa	gcg	aat	caa		864													
Ala	Ile	Asn	Lys	Lys	Lys	Asn	Leu	Glu	Gln	Gln	Leu	Glu	Ala	Asn	Gln															
		275				280						285																		
gct	aaa	ata	aaa	gaa	gca	gaa	aca	ttg	caa	ctt	aaa	cac	ggt	gac	aca		912													
Ala	Lys	Ile	Lys	Glu	Ala	Glu	Thr	Leu	Gln	Leu	Lys	His	Gly	Asp	Thr															
	290					295					300																			
tta	ccg	att	tcg	gct	gga	ttc	ttt	att	att	aat	cca	ttt	gag	gtt	gtt		960													
Leu	Pro	Ile	Ser	Ala	Gly	Phe	Phe	Ile	Ile	Asn	Pro	Phe	Glu	Val	Val															
	305				310					315					320															

tat tat gca ggc ggc aca gca aac gaa ttt cgt cat ttt gct gga agc	1008
Tyr Tyr Ala Gly Gly Thr Ala Asn Glu Phe Arg His Phe Ala Gly Ser	
325 330 335	
tac gca gtg caa tgg gaa atg att aat tat gcg att gat tat caa att	1056
Tyr Ala Val Gln Trp Glu Met Ile Asn Tyr Ala Ile Asp Tyr Gln Ile	
340 345 350	
cca aga tat aac ttt tat ggc att agt ggt gat ttt tca gaa gat gca	1104
Pro Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala	
355 360 365	
gaa gat gca ggt gtg ata aaa ttt aaa aaa ggc tat aat gca gaa gta	1152
Glu Asp Ala Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Glu Val	
370 375 380	
ata gaa tat gtc ggt gat ttt att aag cct ata aac aaa cct gcc tat	1200
Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Ala Tyr	
385 390 395 400	
aca gtc tac tta aaa tta aag caa tta aaa gac aag ata aaa aga taa	1248
Thr Val Tyr Leu Lys Leu Lys Gln Leu Lys Asp Lys Ile Lys Arg	
405 410 415	
gatatagcaa agagaagggg atttattggt atgaaattta cagagttaa	1297

<210> 49
 <211> 415
 <212> PRT
 <213> Staphylococcus schleiferi femA

<400> 49

Thr Thr Ala Glu Phe Gly Ala Phe Thr Asp Gln Met Pro Tyr Ser His	
1 5 10 15	
Phe Thr Gln Met Val Gly Asn Tyr Glu Leu Lys Val Ala Glu Gly Val	
20 25 30	
Glu Thr His Leu Val Gly Ile Lys Asp Asn Asn Asn Asn Val Leu Ala	
35 40 45	
Ala Cys Leu Leu Thr Ala Val Pro Val Met Lys Phe Phe Lys Tyr Phe	
50 55 60	
Tyr Ser Asn Arg Gly Pro Val Met Asp Tyr Glu Asn Lys Glu Leu Val	
65 70 75 80	
His Phe Phe Phe Asn Glu Leu Ser Lys Tyr Val Lys Lys Tyr His Ala	
85 90 95	

Leu Tyr Leu Arg Val Asp Pro Tyr Leu Pro Met Leu Lys Arg Asn His
 100 105 110

Asp Gly Glu Val Ile Glu Arg Tyr Gly Ser Asp Trp Phe Phe Asp Lys
 115 120 125

Met Ala Glu Leu Asn Phe Glu His Glu Gly Phe Thr Thr Gly Phe Asp
 130 135 140

Thr Ile Arg Gln Ile Arg Phe His Ser Val Leu Asp Val Glu Asn Lys
 145 150 155 160

Thr Ser Lys Asp Ile Leu Asn Gln Met Asp Asn Leu Arg Lys Arg Asn
 165 170 175

Thr Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Tyr Leu Asn Glu
 180 185 190

Asp Glu Leu His Ile Phe Arg Ser Phe Met Glu Asp Thr Ser Glu Thr
 195 200 205

Lys Asp Phe Val Asp Arg Asp Asp Asp Phe Tyr Tyr His Arg Met Lys
 210 215 220

Tyr Tyr Lys Asp Arg Val Arg Val Pro Leu Ala Tyr Ile Asp Phe Asn
 225 230 235 240

Ala Tyr Leu Ala Glu Leu Asn Thr Glu Ala Gln Asp Phe Lys Lys Glu
 245 250 255

Ile Ala Lys Ala Asp Lys Asp Ile Asp Lys Arg Pro Glu Asn Gln Lys
 260 265 270

Ala Ile Asn Lys Lys Lys Asn Leu Glu Gln Gln Leu Glu Ala Asn Gln
 275 280 285

Ala Lys Ile Lys Glu Ala Glu Thr Leu Gln Leu Lys His Gly Asp Thr
 290 295 300

Leu Pro Ile Ser Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val
 305 310 315 320

Tyr Tyr Ala Gly Gly Thr Ala Asn Glu Phe Arg His Phe Ala Gly Ser
325 330 335

Tyr Ala Val Gln Trp Glu Met Ile Asn Tyr Ala Ile Asp Tyr Gln Ile
340 345 350

Pro Arg Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala
355 360 365

Glu Asp Ala Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Glu Val
370 375 380

Ile Glu Tyr Val Gly Asp Phe Ile Lys Pro Ile Asn Lys Pro Ala Tyr
385 390 395 400

Thr Val Tyr Leu Lys Leu Lys Gln Leu Lys Asp Lys Ile Lys Arg
405 410 415

<210> 50
<211> 1284
<212> DNA
<213> Staphylococcus sciuri femA

<220>
<221> CDS
<222> (1)..(1233)

<400> 50	
aca ctg gaa ttt gaa gct ttt aca aat aaa atg ccg tac gcg cat ttt	48
Thr Leu Glu Phe Glu Ala Phe Thr Asn Lys Met Pro Tyr Ala His Phe	
1 5 10 15	
aca caa gca gta ggt aat tat gaa tta aaa aca tct gaa ggt act tca	96
Thr Gln Ala Val Gly Asn Tyr Glu Leu Lys Thr Ser Glu Gly Thr Ser	
20 25 30	
aca cat tta gta ggg gtc aaa gat aat caa ggt gaa gta tta gct gcg	144
Thr His Leu Val Gly Val Lys Asp Asn Gln Gly Glu Val Leu Ala Ala	
35 40 45	
tgt ctg tta aca agt gta cca gtt atg aag aaa ttt aat tac ttt tac	192
Cys Leu Leu Thr Ser Val Pro Val Met Lys Lys Phe Asn Tyr Phe Tyr	
50 55 60	
tca aat aga gga cca gta atg gat tat gac aac aaa gaa ctt gtt gac	240
Ser Asn Arg Gly Pro Val Met Asp Tyr Asp Asn Lys Glu Leu Val Asp	
65 70 75 80	
ttt ttc ttt aaa gaa atc gtg agc tat tta aaa agt tat aaa gga tta	288
Phe Phe Phe Lys Glu Ile Val Ser Tyr Leu Lys Ser Tyr Lys Gly Leu	

85	90	95	
ttc ttt aga atc gat cct tac ttg cca tat caa cta aga gat cat gat Phe Phe Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Leu Arg Asp His Asp 100 105 110			336
ggc aat att aaa aaa tca ttc aac cgt gat ggt tta att aaa caa ttt Gly Asn Ile Lys Lys Ser Phe Asn Arg Asp Gly Leu Ile Lys Gln Phe 115 120 125			384
gaa tca tta ggt tat gaa cac caa ggc ttc aca act ggt ttc cac cca Glu Ser Leu Gly Tyr Glu His Gln Gly Phe Thr Gly Phe His Pro 130 135 140			432
ata cat caa att aga tgg cat tct gta ctt gat tta gaa agt atg gac Ile His Gln Ile Arg Trp His Ser Val Leu Asp Leu Glu Ser Met Asp 145 150 155 160			480
gaa aag acg ctc atc aag aac atg gac agt tta aga aaa aga aat act Glu Lys Thr Leu Ile Lys Asn Met Asp Ser Leu Arg Lys Arg Asn Thr 165 170 175			528
aaa aaa gtt caa aaa aat ggt gtt aaa gtt cgt ttt cta tct aaa gat Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Lys Asp 180 185 190			576
gaa atg ccg ata ttc cgt caa ttt atg gaa gat act aca gag aag aaa Glu Met Pro Ile Phe Arg Gln Phe Met Glu Asp Thr Thr Glu Lys Lys 195 200 205			624
gat ttc aac gat cgt ggc gat gac ttc tat tac aat aga tta aaa tac Asp Phe Asn Asp Arg Gly Asp Asp Phe Tyr Tyr Asn Arg Leu Lys Tyr 210 215 220			672
ttt gaa aat gta aag att cct tta gca tat ata gac ttt gaa act tac Phe Glu Asn Val Lys Ile Pro Leu Ala Tyr Ile Asp Phe Glu Thr Tyr 225 230 235 240			720
att cca caa tta gaa aaa gaa cat gaa caa tac aac aaa gat att gca Ile Pro Gln Leu Glu Lys Glu His Glu Gln Tyr Asn Lys Asp Ile Ala 245 250 255			768
aaa gct gaa aaa gat tta gaa aag aaa cca gat aat caa aaa acg att Lys Ala Glu Lys Asp Leu Glu Lys Lys Pro Asp Asn Gln Lys Thr Ile 260 265 270			816
aat aaa ata gac aac tta aaa caa caa aga gaa gca aat gaa gct aaa Asn Lys Ile Asp Asn Leu Lys Gln Gln Arg Glu Ala Asn Glu Ala Lys 275 280 285			864
tta gaa gaa gca ctt caa cta caa caa gaa cat ggt gat aca tta cca Leu Glu Glu Ala Leu Gln Leu Gln Gln Glu His Gly Asp Thr Leu Pro 290 295 300			912
ata gca gct ggt ttc ttt att att aat cca ttt gaa gtt gta tat tat Ile Ala Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val Tyr Tyr 305 310 315 320			960

gca ggt ggt tca tcg aat gaa tat cgt cac ttt gca ggt agt tat gca 1008
Ala Gly Gly Ser Ser Asn Glu Tyr Arg His Phe Ala Gly Ser Tyr Ala
325 330 335

att cag tgg gaa atg att aaa tac gcg tta gat cac aac att gac cgt 1056
Ile Gln Trp Glu Met Ile Lys Tyr Ala Leu Asp His Asn Ile Asp Arg
340 345 350

tat aac ttc tat ggt atc agc gga gac ttc tca gaa gat gca cct gat 1104
Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala Pro Asp
355 360 365

gtt ggc gtt att aaa ttt aaa aaa ggt tac aat gca gat gtt tat gaa 1152
Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val Tyr Glu
370 375 380

tat att ggt gat ttc gtt aaa cca att aat aaa cca gcg tac aaa gca 1200
Tyr Ile Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Ala Tyr Lys Ala
385 390 395 400

tat aca aca cta aaa aaa gta tta aaa aaa taa atgattttca gtaagagagg 1253
Tyr Thr Thr Leu Lys Lys Val Leu Lys Lys
405 410

aatttagata atatgaaatt tacagagtta a 1284

<210> 51
<211> 410
<212> PRT
<213> Staphylococcus sciuri femA

<400> 51

Thr Leu Glu Phe Glu Ala Phe Thr Asn Lys Met Pro Tyr Ala His Phe
1 5 10 15

Thr Gln Ala Val Gly Asn Tyr Glu Leu Lys Thr Ser Glu Gly Thr Ser
20 25 30

Thr His Leu Val Gly Val Lys Asp Asn Gln Gly Glu Val Leu Ala Ala
35 40 45

Cys Leu Leu Thr Ser Val Pro Val Met Lys Lys Phe Asn Tyr Phe Tyr
50 55 60

Ser Asn Arg Gly Pro Val Met Asp Tyr Asp Asn Lys Glu Leu Val Asp
65 70 75 80

Phe Phe Phe Lys Glu Ile Val Ser Tyr Leu Lys Ser Tyr Lys Gly Leu
85 90 95

Phe Phe Arg Ile Asp Pro Tyr Leu Pro Tyr Gln Leu Arg Asp His Asp
100 105 110

Gly Asn Ile Lys Lys Ser Phe Asn Arg Asp Gly Leu Ile Lys Gln Phe
115 120 125

Glu Ser Leu Gly Tyr Glu His Gln Gly Phe Thr Thr Gly Phe His Pro
130 135 140

Ile His Gln Ile Arg Trp His Ser Val Leu Asp Leu Glu Ser Met Asp
145 150 155 160

Glu Lys Thr Leu Ile Lys Asn Met Asp Ser Leu Arg Lys Arg Asn Thr
165 170 175

Lys Lys Val Gln Lys Asn Gly Val Lys Val Arg Phe Leu Ser Lys Asp
180 185 190

Glu Met Pro Ile Phe Arg Gln Phe Met Glu Asp Thr Thr Glu Lys Lys
195 200 205

Asp Phe Asn Asp Arg Gly Asp Asp Phe Tyr Tyr Asn Arg Leu Lys Tyr
210 215 220

Phe Glu Asn Val Lys Ile Pro Leu Ala Tyr Ile Asp Phe Glu Thr Tyr
225 230 235 240

Ile Pro Gln Leu Glu Lys Glu His Glu Gln Tyr Asn Lys Asp Ile Ala
245 250 255

Lys Ala Glu Lys Asp Leu Glu Lys Lys Pro Asp Asn Gln Lys Thr Ile
260 265 270

Asn Lys Ile Asp Asn Leu Lys Gln Gln Arg Glu Ala Asn Glu Ala Lys
275 280 285

Leu Glu Glu Ala Leu Gln Leu Gln Gln Glu His Gly Asp Thr Leu Pro
290 295 300

Ile Ala Ala Gly Phe Phe Ile Ile Asn Pro Phe Glu Val Val Tyr Tyr
305 310 315 320

Ala Gly Gly Ser Ser Asn Glu Tyr Arg His Phe Ala Gly Ser Tyr Ala
 325 330 335

Ile Gln Trp Glu Met Ile Lys Tyr Ala Leu Asp His Asn Ile Asp Arg
 340 345 350

Tyr Asn Phe Tyr Gly Ile Ser Gly Asp Phe Ser Glu Asp Ala Pro Asp
 355 360 365

Val Gly Val Ile Lys Phe Lys Lys Gly Tyr Asn Ala Asp Val Tyr Glu
 370 375 380

Tyr Ile Gly Asp Phe Val Lys Pro Ile Asn Lys Pro Ala Tyr Lys Ala
 385 390 395 400

Tyr Thr Thr Leu Lys Lys Val Leu Lys Lys
 405 410

<210> 52
 <211> 1343
 <212> DNA
 <213> Staphylococcus hominis femA

<220>
 <221> CDS
 <222> (64)..(1317)

<400> 52
 taaaatttta aaattagtca actcaaatta aataaagatt ctaaattagg agttatagag 60
 ata atg aag ttt aca aat tta aca gct aca gaa ttt ggc gat ttt act 108
 Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asp Phe Thr
 1 5 10 15
 gaa aaa atg cca tat agc cat ttt aca cag atg act gaa aat tat gag 156
 Glu Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu
 20 25 30
 tta aaa gtt gct gag aaa act gaa act cat tta gta gga att aaa aat 204
 Leu Lys Val Ala Glu Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn
 35 40 45
 aaa gat aat gaa gtc att gct gct tgt atg cta act gct gta ccc gtt 252
 Lys Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val
 50 55 60
 atg aaa att ttt aaa tat ttt tat tca aat cgt ggt cca gtc att gat 300
 Met Lys Ile Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp
 65 70 75

tat gaa aac aaa gaa ctc gtt cac ttt ttc ttt aac gaa tta agt aaa	348
Tyr Glu Asn Lys Glu Leu Val His Phe Phe Phe Asn Glu Leu Ser Lys	
80 85 90 95	
tat tta aaa caa caa cat tgt tta tat gta cgt ata gac cct tat ttg	396
Tyr Leu Lys Gln Gln His Cys Leu Tyr Val Arg Ile Asp Pro Tyr Leu	
100 105 110	
cct tat caa tat cgt aat cat gat ggt gat att aca gga aat gct ggg	444
Pro Tyr Gln Tyr Arg Asn His Asp Gly Asp Ile Thr Gly Asn Ala Gly	
115 120 125	
aat gat tgg ttc ttc gat aaa atg aaa caa tta gga tat caa cac gaa	492
Asn Asp Trp Phe Phe Asp Lys Met Lys Gln Leu Gly Tyr Gln His Glu	
130 135 140	
ggg ttt aca aca gga ttt gat cca ata tta caa att cgg ttc cat tca	540
Gly Phe Thr Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser	
145 150 155	
gtt tta aat tta aag gat aaa act gct aaa gat gta tta aat gga atg	588
Val Leu Asn Leu Lys Asp Lys Thr Ala Lys Asp Val Leu Asn Gly Met	
160 165 170 175	
gat agt tta cga aaa aga aat act aaa aaa gtc caa aaa aat ggt gtt	636
Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val	
180 185 190	
aaa gta aga ttt ctt act aaa gaa gaa tta cct att ttc aga tca ttt	684
Lys Val Arg Phe Leu Thr Lys Glu Glu Leu Pro Ile Phe Arg Ser Phe	
195 200 205	
atg gaa gat aca tca gag act aaa gaa ttt tct gat aga gag gat agt	732
Met Glu Asp Thr Ser Glu Thr Lys Glu Phe Ser Asp Arg Glu Asp Ser	
210 215 220	
ttt tac tat aat cga ttt gat cat ttt aaa gat aga gta tta gta cct	780
Phe Tyr Tyr Asn Arg Phe Asp His Phe Lys Asp Arg Val Leu Val Pro	
225 230 235	
ctc gca tat ata aaa ttt gat gaa tat ctt gaa gaa ctt cat gca gaa	828
Leu Ala Tyr Ile Lys Phe Asp Glu Tyr Leu Glu Glu Leu His Ala Glu	
240 245 250 255	
cgt cag aca tta aat aaa gac tta aac aaa gct cta aaa gat att gaa	876
Arg Gln Thr Leu Asn Lys Asp Leu Asn Lys Ala Leu Lys Asp Ile Glu	
260 265 270	
aaa cga cca gat aac aaa aaa gca caa aat aaa aaa ata aat tta gaa	924
Lys Arg Pro Asp Asn Lys Lys Ala Gln Asn Lys Lys Ile Asn Leu Glu	
275 280 285	
cag caa tta aaa gca aat gag caa aaa att gat gaa gca aca caa ctt	972
Gln Gln Leu Lys Ala Asn Glu Gln Lys Ile Asp Glu Ala Thr Gln Leu	
290 295 300	
caa tta gaa cat ggt aac gaa tta cca ata tct gct gga ttc ttc ttt	1020

Gln Leu Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe
 305 310 315
 att aat cca ttt gaa gtt gta tat tat gca ggt gga acg tca aat aaa 1068
 Ile Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys
 320 325 330 335
 tat aga cac ttc gct gga agt tat gca gtt caa tgg act atg att aat 1116
 Tyr Arg His Phe Ala Gly Ser Tyr Ala Val Gln Trp Thr Met Ile Asn
 340 345 350
 tat gca att gat cat ggc att gac cgt tat aat ttt tat ggg att agt 1164
 Tyr Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser
 355 360 365
 ggt cat ttt aca gat gat gct gaa gat gca ggt gtt gta aaa ttt aaa 1212
 Gly His Phe Thr Asp Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys
 370 375 380
 aaa gga ttt aat gca gat gta att gaa tat gtt ggt gat ttc gtt aaa 1260
 Lys Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys
 385 390 395
 cct ata aat aaa cca atg tat tca cta tat aca aca ctt aaa aaa att 1308
 Pro Ile Asn Lys Pro Met Tyr Ser Leu Tyr Thr Thr Leu Lys Lys Ile
 400 405 410 415
 aaa aag aga ttgaattaag aggggaatag tgagaa 1343
 Lys Lys Arg

<210> 53
 <211> 418
 <212> PRT
 <213> Staphylococcus hominis femA

<400> 53

Met Lys Phe Thr Asn Leu Thr Ala Thr Glu Phe Gly Asp Phe Thr Glu
 1 5 10 15

Lys Met Pro Tyr Ser His Phe Thr Gln Met Thr Glu Asn Tyr Glu Leu
 20 25 30

Lys Val Ala Glu Lys Thr Glu Thr His Leu Val Gly Ile Lys Asn Lys
 35 40 45

Asp Asn Glu Val Ile Ala Ala Cys Met Leu Thr Ala Val Pro Val Met
 50 55 60

Lys Ile Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Tyr
 65 70 75 80

Glu Asn Lys Glu Leu Val His Phe Phe Phe Asn Glu Leu Ser Lys Tyr
85 90 95

Leu Lys Gln Gln His Cys Leu Tyr Val Arg Ile Asp Pro Tyr Leu Pro
100 105 110

Tyr Gln Tyr Arg Asn His Asp Gly Asp Ile Thr Gly Asn Ala Gly Asn
115 120 125

Asp Trp Phe Phe Asp Lys Met Lys Gln Leu Gly Tyr Gln His Glu Gly
130 135 140

Phe Thr Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser Val
145 150 155 160

Leu Asn Leu Lys Asp Lys Thr Ala Lys Asp Val Leu Asn Gly Met Asp
165 170 175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
180 185 190

Val Arg Phe Leu Thr Lys Glu Glu Leu Pro Ile Phe Arg Ser Phe Met
195 200 205

Glu Asp Thr Ser Glu Thr Lys Glu Phe Ser Asp Arg Glu Asp Ser Phe
210 215 220

Tyr Tyr Asn Arg Phe Asp His Phe Lys Asp Arg Val Leu Val Pro Leu
225 230 235 240

Ala Tyr Ile Lys Phe Asp Glu Tyr Leu Glu Glu Leu His Ala Glu Arg
245 250 255

Gln Thr Leu Asn Lys Asp Leu Asn Lys Ala Leu Lys Asp Ile Glu Lys
260 265 270

Arg Pro Asp Asn Lys Lys Ala Gln Asn Lys Lys Ile Asn Leu Glu Gln
275 280 285

Gln Leu Lys Ala Asn Glu Gln Lys Ile Asp Glu Ala Thr Gln Leu Gln
290 295 300

Leu Glu His Gly Asn Glu Leu Pro Ile Ser Ala Gly Phe Phe Phe Ile
 305 310 315 320

Asn Pro Phe Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Lys Tyr
 325 330 335

Arg His Phe Ala Gly Ser Tyr Ala Val Gln Trp Thr Met Ile Asn Tyr
 340 345 350

Ala Ile Asp His Gly Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
 355 360 365

His Phe Thr Asp Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys Lys
 370 375 380

Gly Phe Asn Ala Asp Val Ile Glu Tyr Val Gly Asp Phe Val Lys Pro
 385 390 395 400

Ile Asn Lys Pro Met Tyr Ser Leu Tyr Thr Thr Leu Lys Lys Ile Lys
 405 410 415

Lys Arg

<210> 54
 <211> 1371
 <212> DNA
 <213> Staphylococcus saprophyticus femA

<220>
 <221> CDS
 <222> (64)..(1326)

<400> 54
 acttgtttag attagaatta aactcgaaaa tagaactata gataaatagg agtatataaa 60

 aaa atg aaa ttt acg aat tta act gca aaa gag ttc ggt gca ttt acg 108
 Met Lys Phe Thr Asn Leu Thr Ala Lys Glu Phe Gly Ala Phe Thr
 1 5 10 15

 gat aaa atg ccg aat agt cat ttt acg caa atg gtt gga aat tat gaa 156
 Asp Lys Met Pro Asn Ser His Phe Thr Gln Met Val Gly Asn Tyr Glu
 20 25 30

 ttg aaa att gca gaa agt aca gaa aca cac cta gta ggt att aag aat 204
 Leu Lys Ile Ala Glu Ser Thr Glu Thr His Leu Val Gly Ile Lys Asn
 35 40 45

aat gat aat gaa gta att gca gca tgt tta ctt aca gct gtt cct gtt	252
Asn Asp Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Ala Val Pro Val	
50 55 60	
atg aaa ttc ttc aag tat ttt tat tcc aat aga ggt cca gtc ata gat	300
Met Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp	
65 70 75	
ttt gaa aat aaa gaa ctc gta cat tac ttc ttt aac gaa tta gca aaa	348
Phe Glu Asn Lys Glu Leu Val His Tyr Phe Phe Asn Glu Leu Ala Lys	
80 85 90 95	
tat gta aaa aaa cat aat gcc tta tat tta cga gta gat cct tat ctt	396
Tyr Val Lys Lys His Asn Ala Leu Tyr Leu Arg Val Asp Pro Tyr Leu	
100 105 110	
gct tat caa tat cgt aat cat gat ggt gaa gta tta gca aat gcg ggt	444
Ala Tyr Gln Tyr Arg Asn His Asp Gly Glu Val Leu Ala Asn Ala Gly	
115 120 125	
cac gat tgg att ttt gat aaa atg aaa caa ctc ggt tat aag cat gaa	492
His Asp Trp Ile Phe Asp Lys Met Lys Gln Leu Gly Tyr Lys His Glu	
130 135 140	
ggg ttt tta act ggc ttt gac cca ata ctt caa ata aga ttc cat tct	540
Gly Phe Leu Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser	
145 150 155	
ggt tta gat tta gct gga aaa act gct aaa gac gta ctt aat ggt atg	588
Val Leu Asp Leu Ala Gly Lys Thr Ala Lys Asp Val Leu Asn Gly Met	
160 165 170 175	
gat agt tta cgt aaa cga aat act aaa aaa gta cag aaa aat ggt gtg	636
Asp Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val	
180 185 190	
aaa gta aga ttt tta ggt gaa gat gag ttg cca ata ttc cgc tca ttc	684
Lys Val Arg Phe Leu Gly Glu Asp Glu Leu Pro Ile Phe Arg Ser Phe	
195 200 205	
atg gaa gat act tct gaa aca aag gat ttt gac gat aga gat gac gat	732
Met Glu Asp Thr Ser Glu Thr Lys Asp Phe Asp Asp Arg Asp Asp Asp	
210 215 220	
ttt tat tat aat agg tta aga tat tat aaa gat cgt gtg ctt gtc cca	780
Phe Tyr Tyr Asn Arg Leu Arg Tyr Tyr Lys Asp Arg Val Leu Val Pro	
225 230 235	
tta gct tat atg gat ttt gat gaa tat ata aca gaa tta aag gct gaa	828
Leu Ala Tyr Met Asp Phe Asp Glu Tyr Ile Thr Glu Leu Lys Ala Glu	
240 245 250 255	
cgc gaa gta tta agt aaa gat ata aat aaa gca gtt aag gat ata gaa	876
Arg Glu Val Leu Ser Lys Asp Ile Asn Lys Ala Val Lys Asp Ile Glu	
260 265 270	
aaa aga cca gaa aat aaa aaa gcg tat aat aaa aaa gaa aat tta gaa	924

Lys	Arg	Pro	Glu	Asn	Lys	Lys	Ala	Tyr	Asn	Lys	Lys	Glu	Asn	Leu	Glu		
			275					280					285				
caa	caa	ctg	att	gca	aac	caa	caa	aaa	ata	gat	gaa	gcc	act	gcg	tta	972	
Gln	Gln	Leu	Ile	Ala	Asn	Gln	Gln	Lys	Ile	Asp	Glu	Ala	Thr	Ala	Leu		
		290					295					300					
caa	gag	aag	cat	ggt	aac	gaa	tta	ccg	att	tct	gca	gct	tac	ttt	att	1020	
Gln	Glu	Lys	His	Gly	Asn	Glu	Leu	Pro	Ile	Ser	Ala	Ala	Tyr	Phe	Ile		
	305					310					315						
att	aat	cct	tat	gaa	gtc	gtt	tac	tat	gca	ggt	ggt	aca	tct	aat	gaa	1068	
Ile	Asn	Pro	Tyr	Glu	Val	Val	Tyr	Tyr	Ala	Gly	Gly	Thr	Ser	Asn	Glu		
320					325					330					335		
ttt	aga	cat	ttt	gct	ggt	agt	tat	gca	ata	caa	tgg	aag	atg	att	aat	1116	
Phe	Arg	His	Phe	Ala	Gly	Ser	Tyr	Ala	Ile	Gln	Trp	Lys	Met	Ile	Asn		
			340						345					350			
tat	gct	ata	gat	cat	aat	ata	gat	aga	tat	aat	ttt	tat	ggt	att	agt	1164	
Tyr	Ala	Ile	Asp	His	Asn	Ile	Asp	Arg	Tyr	Asn	Phe	Tyr	Gly	Ile	Ser		
			355					360					365				
ggt	cat	ttt	act	gaa	gat	gca	gaa	gat	gca	ggt	gtt	gtt	aaa	ttt	aaa	1212	
Gly	His	Phe	Thr	Glu	Asp	Ala	Glu	Asp	Ala	Gly	Val	Val	Lys	Phe	Lys		
		370				375						380					
aaa	ggt	ttt	aat	gca	gat	gta	gta	gaa	tat	gtt	ggt	gat	ttt	att	aaa	1260	
Lys	Gly	Phe	Asn	Ala	Asp	Val	Val	Glu	Tyr	Val	Gly	Asp	Phe	Ile	Lys		
	385					390					395						
ccg	att	aat	aag	cca	atg	tac	aaa	att	tat	acg	aca	ttg	aaa	aaa	att	1308	
Pro	Ile	Asn	Lys	Pro	Met	Tyr	Lys	Ile	Tyr	Thr	Thr	Leu	Lys	Lys	Ile		
400					405					410					415		
aag	gat	aaa	aag	aaa	taa	acataaatag	aagggaacta	agctagaatg								1356	
Lys	Asp	Lys	Lys	Lys													
			420														
aaattttacag	agtta															1371	

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Lys	Met	Pro	Asn	Ser	His	Phe	Thr	Gln	Met	Val	Gly	Asn	Tyr	Glu	Leu
			20					25					30		

Lys Ile Ala Glu Ser Thr Glu Thr His Leu Val Gly Ile Lys Asn Asn
 35 40 45

Asp Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Ala Val Pro Val Met
 50 55 60

Lys Phe Phe Lys Tyr Phe Tyr Ser Asn Arg Gly Pro Val Ile Asp Phe
 65 70 75 80

Glu Asn Lys Glu Leu Val His Tyr Phe Phe Asn Glu Leu Ala Lys Tyr
 85 90 95

Val Lys Lys His Asn Ala Leu Tyr Leu Arg Val Asp Pro Tyr Leu Ala
 100 105 110

Tyr Gln Tyr Arg Asn His Asp Gly Glu Val Leu Ala Asn Ala Gly His
 115 120 125

Asp Trp Ile Phe Asp Lys Met Lys Gln Leu Gly Tyr Lys His Glu Gly
 130 135 140

Phe Leu Thr Gly Phe Asp Pro Ile Leu Gln Ile Arg Phe His Ser Val
 145 150 155 160

Leu Asp Leu Ala Gly Lys Thr Ala Lys Asp Val Leu Asn Gly Met Asp
 165 170 175

Ser Leu Arg Lys Arg Asn Thr Lys Lys Val Gln Lys Asn Gly Val Lys
 180 185 190

Val Arg Phe Leu Gly Glu Asp Glu Leu Pro Ile Phe Arg Ser Phe Met
 195 200 205

Glu Asp Thr Ser Glu Thr Lys Asp Phe Asp Asp Arg Asp Asp Asp Phe
 210 215 220

Tyr Tyr Asn Arg Leu Arg Tyr Tyr Lys Asp Arg Val Leu Val Pro Leu
 225 230 235 240

Ala Tyr Met Asp Phe Asp Glu Tyr Ile Thr Glu Leu Lys Ala Glu Arg
 245 250 255

Glu Val Leu Ser Lys Asp Ile Asn Lys Ala Val Lys Asp Ile Glu Lys

260

265

270

Arg Pro Glu Asn Lys Lys Ala Tyr Asn Lys Lys Glu Asn Leu Glu Gln
 275 280 285

Gln Leu Ile Ala Asn Gln Gln Lys Ile Asp Glu Ala Thr Ala Leu Gln
 290 295 300

Glu Lys His Gly Asn Glu Leu Pro Ile Ser Ala Ala Tyr Phe Ile Ile
 305 310 315 320

Asn Pro Tyr Glu Val Val Tyr Tyr Ala Gly Gly Thr Ser Asn Glu Phe
 325 330 335

Arg His Phe Ala Gly Ser Tyr Ala Ile Gln Trp Lys Met Ile Asn Tyr
 340 345 350

Ala Ile Asp His Asn Ile Asp Arg Tyr Asn Phe Tyr Gly Ile Ser Gly
 355 360 365

His Phe Thr Glu Asp Ala Glu Asp Ala Gly Val Val Lys Phe Lys Lys
 370 375 380

Gly Phe Asn Ala Asp Val Val Glu Tyr Val Gly Asp Phe Ile Lys Pro
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18